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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,859

DATE: 02/05/2003
TIME: 08:13:12

Input Set : A:\KATO SEQUENCE LISTING.txt
Output Set: N:\CRF4\02052003\J088859.raw

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3 <110> APPLICANT: KATO, Seishi
4      NAGATA, Naoki
5      FUJIMURA, Naoko
6      KOBAYASHI, Midori
7      ITO, Koichi
8      ISHIZUKA, Yoshiko
10 <120> TITLE OF INVENTION: A Method for Producing an Antibody by Gene Immunization
12 <130> FILE REFERENCE: 2002-0400A/LC/00653
14 <140> CURRENT APPLICATION NUMBER: 10/088,859
15 <141> CURRENT FILING DATE: 2002-05-29
17 <150> PRIOR APPLICATION NUMBER: PCT/JP01/06371
18 <151> PRIOR FILING DATE: 2001-07-24
20 <150> PRIOR APPLICATION NUMBER: JP2000-222743
21 <151> PRIOR FILING DATE: 2000-07-24
23 <150> PRIOR APPLICATION NUMBER: JP2000-254407
24 <151> PRIOR FILING DATE: 2000-08-24
26 <160> NUMBER OF SEQ ID NOS: 13
28 <170> SOFTWARE: PatentIn Ver. 2.1
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31 <211> LENGTH: 697
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
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36 <221> NAME/KEY: CDS
37 <222> LOCATION: (151)..(600)
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42 aataaaagtta caactttgaa gagagTTTct gcaagacatg acacAAAGCT gctagcagaa 120
44 aatcaaaacg ctgattaaaa gaagcacggt atg atg acc aaa cat aaa aag tgt 174
45 Met Met Thr Lys His Lys Lys Cys
46           1           5
48 ttt ata att gtt ggt gtt tta ata aca act aat att att act ctg ata 222
49 Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile
50      10          15          20
52 gtt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att 270
53 Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile
54      25          30          35          40
56 ggt ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg 318
57 Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Gly Asp Trp
58      45          50          55
60 aat tca agt aaa tac aac tgt tcc actcaa cat gcc gac cta act ata 366
61 Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
62      60          65          70

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64 att gac aac ata gaa gaa atg aat ttt ctt agg cggttataaa tgc agt 414
65 Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser
66 75 80 85
68 tct gat cac tgg att gga ctg aag atg gca aaa aat cga aca gga caa 462
69 Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln
70 90 95 100
72 tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt 510
73 Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser
74 105 110 115 120
76 gaa gga tgt gcc tac ctc agc gat gat ggt gca gca aca gct aga tgt 558
77 Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys
78 125 130 135
80 tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taa 600
81 Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His
82 140 145
84 gttaatgtct aagataatgg ggaaaataga aaataacatt attaagtgtaa aaccagcaa 660
86 agtactttt taattaaaca aagttcgagt tttgtac 697
89 <210> SEQ ID NO: 2
90 <211> LENGTH: 149
91 <212> TYPE: PRT
92 <213> ORGANISM: Homo sapiens
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97 Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln
98 20 25 30
99 Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr
100 35 40 45
101 Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
102 50 55 60
103 Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn
104 65 70 75 80
105 Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys
106 85 90 95
107 Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr
108 100 105 110
109 Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
110 115 120 125
111 Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys
112 130 135 140
113 Arg Lys Arg Ile His
114 145
118 <210> SEQ ID NO: 3
119 <211> LENGTH: 548
120 <212> TYPE: DNA
121 <213> ORGANISM: Homo sapiens
123 <220> FEATURE:
124 <221> NAME/KEY: CDS
125 <222> LOCATION: (30)..(503)

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130 1 5
132 gc gt ga gc ac gg gg aa gt ct gc ta cg ag ac tt ca tc 101
133 Ala Val Glu Ala Thr Gly Glu Lys Val Leu Arg Tyr Glu Thr Phe Ile
134 10 15 20
136 agt gac gtg ctg cag cgg gac ttg cga aag gtg ctg gac cat cga gac 149
137 Ser Asp Val Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp
138 25 30 35 40
140 aag gta tat gag cag ctg gcc aaa tac ctt caa ctg aga aat gtc att 197
141 Lys Val Tyr Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile
142 45 50 55
144 gag cga ctc cag gaa gct aag cac tcg gag tta tat atg cag gtg gat .245
145 Glu Arg Leu Gln Glu Ala Lys His Ser Glu Leu Tyr Met Gln Val Asp
146 60 65 70
148 ttg ggc tgt aac ttc ttc gtt gac aca gtg gtc cca gat act tca cgc 293
149 Leu Gly Cys Asn Phe Phe Val Asp Thr Val Val Pro Asp Thr Ser Arg
150 75 80 85
152 atc tat gtg gcc ctg gga tat ggt ttt ttc ctg gag ttg aca ctg gca 341
153 Ile Tyr Val Ala Leu Gly Tyr Gly Phe Phe Leu Glu Leu Thr Leu Ala
154 90 95 100
156 gaa gct ctc aag ttc att gat cgt aag agc tct ctc ctc aca gag ctc 389
157 Glu Ala Leu Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu
158 105 110 115 120
160 agc aac agc ctc acc aag gac tcc atg aat atc aaa gcc cat atc cac 437
161 Ser Asn Ser Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His
162 125 130 135
164 atg ttg cta gag ggg ctt aga gaa cta caa ggc ctg cag aat ttc cca 485
165 Met Leu Leu Glu Gly Leu Arg Glu Leu Gln Gly Leu Gln Asn Phe Pro
166 140 145 150
168 gag aag cct cac cat tga cttctcccc ccatacctcag acattaaaga 533
169 Glu Lys Pro His His
170 155
172 gcctgaatgc ctttg 548
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 157
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 4
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182 1 5 10 15
183 Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
184 20 25 30
185 Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
186 35 40 45
187 Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
188 50 55 60
189 Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp

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190 65          70          75          80
191 Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
192           85           90           95
193 Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
194           100          105          110
195 Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
196           115          120          125
197 Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
198           130          135          140
199 Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
200 145          150          155
203 <210> SEQ ID NO: 5
204 <211> LENGTH: 30
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Artificial Sequence: Synthesized oligonucleotide
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216 <211> LENGTH: 30
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Artificial Sequence: Synthesized oligonucleotide
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228 <211> LENGTH: 28
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Artificial Sequence: Synthesized oligonucleotide
235 <400> SEQUENCE: 7
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238 <210> SEQ ID NO: 8
239 <211> LENGTH: 32
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Artificial Sequence: Synthesized oligonucleotide
246 <400> SEQUENCE: 8
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251 <211> LENGTH: 1643
252 <212> TYPE: DNA
253 <213> ORGANISM: Homo sapiens
255 <220> FEATURE:
256 <221> NAME/KEY: CDS

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257 <222> LOCATION: (25)..(915)
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 262 1 5
 264 cag cag ctg ggc ctc ctg ggg tgt ctt ggc cat ggc gcc ctg gtg ctg 99
 265 Gln Gln Leu Gly Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu
 266 10 15 20 25
 268 caa ctc ctc tcc ttc atg ctc ttg gct ggg gtc ctg gtg gcc atc ctt 147
 269 Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu
 270 30 35 40
 272 gtc caa gtg tcc aag gtc ccc agc tcc cta agt cag gaa caa tcc gag 195
 273 Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu
 274 45 50 55
 276 caa gac gca atc tac cag aac ctg acc cag ctt aaa gct gca gtg ggt 243
 277 Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly
 278 60 65 70
 280 gag ctc tca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc 291
 281 Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
 282 75 80 85
 284 cag ctg aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag 339
 285 Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
 286 90 95 100 105
 288 gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg 387
 289 Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu
 290 110 115 120
 292 cca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc cgg ctg 435
 293 Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
 294 125 130 135
 296 aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc 483
 297 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile
 298 140 145 150
 300 tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg cca gag 531
 301 Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
 302 155 160 165
 304 aaa tcc aag ctg cag gag atc tac cag gag ctg acg gag ctg aag gct 579
 305 Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala
 306 170 175 180 185
 308 gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc tac cag 627
 309 Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln
 310 190 195 200
 312 gag ctg acc cag ctg aag gct gca gtg ggt gag ttg cca gac cag tcc 675
 313 Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser
 314 205 210 215
 316 aag cag cag caa atc tat caa gaa ctg acc gat ttg aag act gca ttt 723
 317 Lys Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe
 318 220 225 230
 320 gaa cgc ctg tgc cgc cac tgt ccc aag gac tgg aca ttc ttc caa gga 771
 321 Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly

VERIFICATION SUMMARY

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